1

SEQUENCE LISTING

<110> EISAI CO., LTD.

<120> Screening method

<130> E1-A0410Y1P

<150> JP 2004-31591
<151> 2004-02-09

<150> JP 2004-368509
<151> 2004-12-20

<160> 14

<170> PatentIn version 3.1

<210> 1
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(429)
<223>

<400> 1

```
atg gcc agg tac atg ctg ctg ctg ctc ctg gcg gta tgg gtg ctg acc      48
Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr
1               5                   10                  15

ggg gag ctg tgg ccg gga gct gag gcc cgg gca gcg cct tac ggg gtc      96
Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
            20                  25                  30

agg ctt tgc ggc cga gaa ttc atc cga gca gtc atc ttc acc tgc ggg     144
Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
        35                  40                  45

ggc tcc cgg tgg aga cga tca gac atc ctg gcc cac gag gct atg gga     192
Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
    50                  55                  60

gat acc ttc ccg gat gca gat gct gat gaa gac agt ctg gca ggc gag     240
Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu
```

| | 65 | | 70 | | | 75 | | | 80 | |

```
          65                  70                  75                  80

ctg gat gag gcc atg ggg tcc agc gag tgg ctg gcc ctg acc aag tca        288
Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser
                85                  90                  95

ccc cag gcc ttt tac agg ggg cga ccc agc tgg caa gga acc cct ggg        336
Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly
                100                 105                 110

gtt ctt cgg ggc agc cga gat gtc ctg gct ggc ctt tcc agc agc tgc        384
Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys
                115                 120                 125

tgc aag tgg ggg tgt agc aaa agt gaa atc agt agc ctt tgc tag           429
Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
                130                 135                 140
```

<210> 2
<211> 142
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Ala Arg Tyr Met Leu Leu Leu Leu Ala Val Trp Val Leu Thr
1               5                   10                  15


Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
                20                  25                  30


Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
        35                  40                  45


Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
        50                  55                  60


Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu
65                  70                  75                  80


Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser
                85                  90                  95
```

```
Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly
        100                 105                 110


Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys
        115                 120                 125


Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
        130                 135                 140
```

<210> 3
<211> 1857
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (361)..(1770)
<223>

<400> 3

```
gatttgggga gttatgcgcc agtgccccag tgaccgcggg acacggagag gggaagtctg      60

cgttgtacat aaggacctag ggactccgag cttggcctga gaacccttgg acgccgagtg     120

cttgccttac gggctgcact cctcaactct gctccaaagc agccgctgag ctcaactcct     180

gcgtccaggg cgttcgctgc gcgccaggac gcgcttagta cccagttcct gggctctctc     240

ttcagtagct gctttgaaag ctcccacgca cgtcccgcag gctagcctgg caacaaaact     300

ggggtaaacc gtgttatctt aggtcttgtc ccccagaaca tgacctagag gtacctgcgc     360
```

```
atg cag atg gcc gat gca gcc acg ata gcc acc atg aat aag gca gca      408
Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
1               5                   10                  15


ggc ggg gac aag cta gca gaa ctc ttc agt ctg gtc ccg gac ctt ctg      456
Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
            20                  25                  30


gag gcg gcc aac acg agt ggt aac gcg tcg ctg cag ctt ccg gac ttg      504
Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
        35                  40                  45
```

```
tgg tgg gag ctg ggg ctg gag ttg ccg gac ggc gcg ccg cca gga cat    552
Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His
    50              55              60


ccc ccg ggc agc ggc ggg gca gag agc gcg gac aca gag gcc cgg gtg    600
Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val
65              70              75              80


cgg att ctc atc agc gtg gtg tac tgg gtg gtg tgc gcc ctg ggg ttg    648
Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu
                85              90              95


gcg ggc aac ctg ctg gtt ctc tac ctg atg aag agc atg cag ggc tgg    696
Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp
            100             105             110


cgc aag tcc tct atc aac ctc ttc gtc acc aac ctg gcg ctg acg gac    744
Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp
        115             120             125


ttt cag ttt gtg ctc acc ctg ccc ttc tgg gcg gtg gag aac gct ctt    792
Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu
    130             135             140


gac ttc aaa tgg ccc ttc ggc aag gcc atg tgt aag atc gtg tcc atg    840
Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met
145             150             155             160


gtg acg tcc atg aac atg tac gcc agc gtg ttc ttc ctc act gcc atg    888
Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met
                165             170             175


agt gtg acg cgc tac cat tcg gtg gcc tcg gct ctg aag agc cac cgg    936
Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg
            180             185             190


acc cga gga cac ggc cgg ggc gac tgc tgc ggc cgg agc ctg ggg gac    984
Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp
        195             200             205


agc tgc tgc ttc tcg gcc aag gcg ctg tgt gtg tgg atc tgg gct ttg   1032
Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu
        210             215             220


gcc gcg ctg gcc tcg ctg ccc agt gcc att ttc tcc acc acg gtc aag   1080
Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys
225             230             235             240
```

```
gtg atg ggc gag gag ctg tgc ctg gtg cgt ttc ccg gac aag ttg ctg      1128
Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu
            245                 250                 255

ggc cgc gac agg cag ttc tgg ctg ggc ctc tac cac tcg cag aag gtg      1176
Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val
            260                 265                 270

ctg ttg ggc ttc gtg ctg ccg ctg ggc atc att atc ttg tgc tac ctg      1224
Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu
            275                 280                 285

ctg ctg gtg cgc ttc atc gcc gac cgc cgc gcg gcg ggg acc aaa gga      1272
Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly
        290                 295                 300

ggg gcc gcg gta gcc gga gga cgc ccg acc gga gcc agc gcc cgg aga      1320
Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
305                 310                 315                 320

ctg tcg aag gtc acc aaa tca gtg acc atc gtt gtc ctg tcc ttc ttc      1368
Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
            325                 330                 335

ctg tgt tgg ctg ccc aac cag gcg ctc acc acc tgg agc atc ctc atc      1416
Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
            340                 345                 350

aag ttc aac gcg gtg ccc ttc agc cag gag tat ttc ctg tgc cag gta      1464
Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
            355                 360                 365

tac gcg ttc cct gtg agc gtg tgc cta gcg cac tcc aac agc tgc ctc      1512
Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
        370                 375                 380

aac ccc gtc ctc tac tgc ctc gtg cgc cgc gag ttc cgc aag gcg ctc      1560
Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
385                 390                 395                 400

aag agc ctg ctg tgg cgc atc gcg tct cct tcg atc acc agc atg cgc      1608
Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
            405                 410                 415

ccc ttc acc gcc act acc aag ccg gag cac gag gat cag ggg ctg cag      1656
Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln
            420                 425                 430
```

```
gcc ccg gcg ccg ccc cac gcg gcc gcg gag ccg gac ctg ctc tac tac      1704
Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
        435             440             445


cca cct ggc gtc gtg gtc tac agc ggg ggg cgc tac gac ctg ctg ccc      1752
Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
    450             455             460


agc agc tct gcc tac tga cgcaggcctc aggcccaggg cgcgccgtcg             1800
Ser Ser Ser Ala Tyr
.465


gggcaaggtg gccttccccg ggcggtaaag aggtgaaagg atgaaggagg gctgggg       1857
```


<210> 4
<211> 469
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
1               5               10              15


Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
            20              25              30


Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
        35              40              45


Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His
    50              55              60


Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val
65              70              75              80


Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu
            85              90              95


Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp
```

                        100   105   110

Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp
        115   120   125

Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu
        130   135   140

Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met
145   150   155   160

Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met
                165   170   175

Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg
            180   185   190

Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp
            195   200   205

Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu
        210   215   220

Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys
225   230   235   240

Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu
                245   250   255

Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val
            260   265   270

Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu
        275   280   285

Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly

```
                290                    295                    300


        Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
        305                    310                    315                    320


        Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
                        325                    330                    335


        Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
                        340                    345                    350


        Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
                        355                    360                    365


        Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
            370                    375                    380


        Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
        385                    390                    395                    400


        Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
                        405                    410                    415


        Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln
                        420                    425                    430


        Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
                        435                    440                    445


        Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
            450                    455                    460


        Ser Ser Ser Ala Tyr
        465


        <210> 5
```

<210> 5
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> A sense primer

<400> 5
gatatcgccg ccaccatgca gatggccgat gcagccac   38

<210> 6
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> An antisense primer

<400> 6
gatatctcag taggcagagc tgctgggc   28

<210> 7
<211> 5020
<212> DNA
<213> Plasmid

<400> 7
ctgcagcctg aatatgggcc aaacaggata tctgtggtaa gcagttcctg ccccggctca   60

gggccaagaa cagatggaac agctgaatat gggccaaaca ggatatctgt ggtaagcagt   120

tcctgccccg gctcagggcc aagaacagat ggtccccaga tgcggtccag ccctcagcag   180

tttctagaga accatcagat gtttccaggg tgccccaagg acctgaaatg accctgtgcc   240

ttatttgaac taaccaatca gttcgcttct cgcttctgtt cgcgcgcttc tgctccccga   300

gctcaataaa agagcccaca acccctcact cggggcgcca gtcctccgat tgactgagtc   360

gcccgggtac ccgtgtatcc aataaaccct cttgcagttg catccgactt gtggtctcgc   420

tgttccttgg gagggtctcc tctgagtgat tgactacccg tcagcggggg tctttcattt   480

gggggctcgt ccgggatcgg gagacccctg cccagggacc accgacccac caccgggagg   540

taagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta   600

```
tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcggacc cgtggtggaa    660

ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccagggac tttggggggcc   720

gtttttgtgg cccgacctga ggaagggagt cgatgtggaa tccgacccg tcaggatatg    780

tggttctggt aggagacgag aacctaaaac agttcccgcc tccgtctgaa tttttgcttt    840

cggtttggaa ccgaagccgc gcgtcttgtc tgctgcagca tcgttctgtg ttgtctctgt    900

ctgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt    960

ttgaccttag atcactggaa agatgtcgag cggctcgctc acaaccagtc ggtagatgtc   1020

aagaagagac gttgggttac cttctgctct gcagaatggc caacctttaa cgtcggatgg   1080

ccgcgagacg gcacctttaa ccgagacctc atcacccagg ttaagatcaa ggtcttttca   1140

cctggcccgc atggacaccc agaccaggtc ccctacatcg tgacctggga agccttggct   1200

tttgaccccc ctccctgggt caagcccttt gtacacccta agcctccgcc tcctcttctt   1260

ccatccgcgc cgtctctccc ccttgaacct cctctttcga ccccgcctca atcctccctt   1320

tatccagccc tcactccttc tctaggcgcc ggccggatcc cagtgtggtg gtacgtagga   1380

attcgccagc acagtggtcg acctgtggaa tgtgtgtcag ttagggtgtg gaaagtcccc   1440

aggctcccca gcaggcagaa gtatgcaaag catgcatctc aattagtcag caaccaggtg   1500

tggaaagtcc ccaggctccc cagcaggcag aagtatgcaa agcatgcatc tcaattagtc   1560

agcaaccata gtcccgcccc taactccgcc catcccgccc ctaactccgc ccagttccgc   1620

ccattctccg ccccatggct gactaatttt ttttatttat gcagaggccg aggccgcctc   1680

ggcctctgag ctattccaga gtagtgagg aggctttttt ggaggcctag gcttttgcaa    1740

acgctgcttg aggctgaagg tgcgttgctg gcgttttttcc ataggctccg cccccctgac   1800

gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg actataaaga   1860

taccaggcgt ttccccctgg aagctccctc gtgcgctctc ctgttccgac cctgccgctt   1920

accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca tagctcacgc   1980

tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc tgggctgtgt gcacgaaccc   2040
```

```
cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc caacccggta   2100

agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag agcgaggtat   2160

gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac tagaaggaca   2220

gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt tggtagctct   2280

tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa gcagcagatt   2340

acgatcgata aaataaaaga ttttatttag tctccagaaa aaggggggaa tgaaagaccc   2400

cacctgtagg tttggcaagc tagcttaagt aacgccattt tgcaaggcat ggaaaaatac   2460

ataactgaga atagagaagt tcagatcaag gtcaggaaca gatggaacag ctgaatatgg   2520

gccaaacagg atatctgtgg taagcagttc ctgccccggc tcagggccaa gaacagatgg   2580

aacagctgaa tatgggccaa acaggatatc tgtggtaagc agttcctgcc ccggctcagg   2640

gccaagaaca gatggtcccc agatgcggtc cagccctcag cagtttctag agaaccatca   2700

gatgtttcca gggtgcccca aggacctgaa atgaccctgt gccttatttg aactaaccaa   2760

tcagttcgct tctcgcttct gttcgcgcgc ttctgctccc cgagctcaat aaaagagccc   2820

acaacccctc actcggggcg ccagtcctcc gattgactga gtcgcccggg tacccgtgta   2880

tccaataaac cctcttgcag ttgcatccga cttgtggtct cgctgttcct tgggagggtc   2940

tcctctgagt gattgactac ccgtcagcgg gggtctttca catgcagcat gtatcaaaat   3000

taatttggtt tttttcctta agtatttaca ttaaatggcc atagttgcat taatgaatcg   3060

gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg   3120

actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc agctcactca aaggcggtaa   3180

tacggttatc cacagaatca ggggataacg caggaaagaa catgtgagca aaaggccagc   3240

aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg ctccgccccc   3300

ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg acaggactat   3360

aaagatacca ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt ccgaccctgc   3420

cgcttaccgg atacctgtcc gcctttctcc cttcgggaag cgtggcgctt tctcatagct   3480
```

```
cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg   3540

aaccccccgt tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc   3600

cggtaagaca cgacttatcg ccactggcag cagccactgg taacaggatt agcagagcga   3660

ggtatgtagg cggtgctaca gagttcttga agtggtggcc taactacggc tacactagaa   3720

ggacagtatt tggtatctgc gctctgctga agccagttac cttcggaaaa agagttggta   3780

gctcttgatc cggcaaacaa accaccgctg gtagcggtgg ttttttttgtt tgcaagcagc   3840

agattacgcg cagaaaaaaa ggatctcaag aagatccttt gatcttttct acggggtctg   3900

acgctcagtg gaacgaaaac tcacgttaag ggattttggt catgagatta tcaaaaagga   3960

tcttcaccta gatccttta aattaaaaat gaagtttgcg gccgcaaatc aatctaaagt   4020

atatatgagt aaacttggtc tgacagttac caatgcttaa tcagtgaggc acctatctca   4080

gcgatctgtc tatttcgttc atccatagtt gcctgactcc ccgtcgtgta gataactacg   4140

atacgggagg gcttaccatc tggccccagt gctgcaatga taccgcgaga cccacgctca   4200

ccggctccag atttatcagc aataaaccag ccagccggaa gggccgagcg cagaagtggt   4260

cctgcaactt tatccgcctc catccagtct attaattgtt gccgggaagc tagagtaagt   4320

agttcgccag ttaatagttt gcgcaacgtt gttgccattg ctacaggcat cgtggtgtca   4380

cgctcgtcgt ttggtatggc ttcattcagc tccggttccc aacgatcaag gcgagttaca   4440

tgatccccca tgttgtgcaa aaaagcggtt agctccttcg gtcctccgat cgttgtcaga   4500

agtaagttgg ccgcagtgtt atcactcatg gttatggcag cactgcataa ttctcttact   4560

gtcatgccat ccgtaagatg cttttctgtg actggtgagt actcaaccaa gtcattctga   4620

gaatagtgta tgcggcgacc gagttgctct tgcccggcgt caacacggga taataccgcg   4680

ccacatagca gaactttaaa agtgctcatc attggaaaac gttcttcggg gcgaaaactc   4740

tcaaggatct taccgctgtt gagatccagt tcgatgtaac ccactcgtgc acccaactga   4800

tcttcagcat cttttacttt caccagcgtt tctgggtgag caaaaacagg aaggcaaaat   4860

gccgcaaaaa agggaataag ggcgacacgg aaatgttgaa tactcatact cttccttttt   4920
```

caatattatt gaagcattta tcagggttat tgtctcatga gcggatacat atttgaatgt   4980

atttagaaaa ataaacaaat aggggttccg cgcacatttc   5020

<210> 8
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> A sense strand for CREx2hb

<400> 8
cccaagcttg atatcgaatt cgacgtcaca gtatgacggc catgggaatt cgacgtcaca   60

gtatgacggc catggggatc ccg   83

<210> 9
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> An antisense strand for CREx2hb

<400> 9
cgggatcccc atggccgtca tactgtgacg tcgaattccc atggccgtca tactgtgacg   60

tcgaattcga tatcaagctt ggg   83

<210> 10
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> A sense strand for CREx2bp

<400> 10
tgcactgcag gaattcccat ggccgtcata ctgtgacgtc gaattcccat ggccgtcata   60

ctgtgacgtc ggatcccg   78

<210> 11
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> An antisense strand for CREx2bp

<400> 11
cgggatccga cgtcacagta tgacggccat gggaattcga cgtcacagta tgacggccat   60

gggaattcct gcagtgca   78

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> A sense primer

<400> 12
tcgactgcag cccatggccg tcatactgtg   30

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> An antisense primer

<400> 13
tgcactgcag gtcggagctg actgttctgg   30

<210> 14
<211> 264
<212> DNA
<213> Artificial Sequence

<220>
<223> Vasoactive intestinal peptide promoter

<400> 14
tcgactgcag cccatggccg tcatactgtg tgacgtcttt cagagcactt tgtgattgct   60

cagtcctaag tataagccct ataaaatgat gggctttgaa atgctggtca gggtagagtg   120

agaagcacca gcaggcagta acagccaacc cttagccatt gctaagggca gagaactggt   180

ggagcctttc tcttactccc aggacttcag cacctaagac agctccaaaa caaaccagaa   240

cagtcagctc cgacctgcag tgca   264